

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims

Claims 1-2 (canceled)

3. (previously presented) The method of claims 127, wherein at least about 100 samples are screened for presence of the one or more component of interest in less than an hour.

4. (previously presented) The method of claim 127, wherein at least about 200 samples are screened for presence of the one or more component of interest in less than an hour.

5. (previously presented) The method of claim 127, wherein at least about 500 samples are screened for presence of the one or more component of interest in less than an hour.

6. (previously presented) The method of claim 127, wherein at least about 1000 samples are screened for the presence of the one or more component of interest in about 1 day.

Claims 7-22 (canceled)

23. (previously presented) The method of claim 127, wherein performing flow injection analysis using electrospray tandem mass spectrometry comprises performing a method selected from the group consisting of neutral loss mass spectrometry and parent ion mass spectrometry.

24. (Original) The method of claim 23, comprising performing the neutral loss mass spectrometry or the parent ion mass spectrometry on a triple quadrupole mass spectrometer.

25. (previously presented) The method of claim 24, wherein performing the neutral loss mass spectrometry comprises:

- (a) scanning the one or more component of interest in a first quadrupole at a specified mass range;
- (b) fragmenting the one or more component of interest in a second quadrupole by collision induced dissociation, thereby producing one or more neutral fragments and one or more daughter ion; and,
- (c) detecting the one or more daughter ion.

26. (previously presented) The method of claim 24, wherein performing the parent ion mass spectrometry comprises:

- (a) scanning the one or more component of interest in a first quadrupole;
- (b) fragmenting the one or more component of interest in a second quadrupole by collision induced dissociation; and,
- (c) scanning a third quadrupole at a specified mass.

Claims 27-71 (canceled)

72. (previously presented) The method of claim 127, wherein step (iii) comprises using centrifugation.

73. (previously presented) The method of claim 127, wherein step (iii) comprises using filtration.

Claims 74-76 (canceled)

77. (previously presented) The method of claim 127, wherein an automatic sampler transports samples from step (iii) to the mass spectrometer for injection and analysis at a rate of at least 100 samples an hour.

78. (previously presented) The method of claim 127 , wherein 5 to 100 samples are pooled before performing flow-injection analysis using electrospray tandem mass spectrometry.

Claims 79-105(canceled)

106. (previously presented) The method of claim 136, wherein at least about 100 samples are screened for presence of the product(s) of an enzymatic reaction or enzyme substrate(s) in less than an hour.

107. (previously presented) The method of claim 136, wherein at least about 200 samples are screened for presence of the product(s) of an enzymatic reaction or enzyme substrate(s) in less than an hour.

108. (previously presented) The method of claim 136, wherein at least about 500 samples are screened for presence of the product(s) of an enzymatic reaction or enzyme substrate(s) in less than an hour.

109. (previously presented) The method of claim 136, wherein at least about 1000 samples are screened for the presence of the product(s) of an enzymatic reaction or enzyme substrate(s) in about 1 day.

Claim 110 (cancelled)

Claims 111-114 (canceled)

115. (previously presented) The method of claim 136, further comprising simultaneously quantifying the amount of the product(s) of an enzyme reaction and the enzyme substrate(s).

116. (previously presented) The method of claim 136, wherein performing flow injection analysis using electrospray tandem mass spectrometry comprises performing a method selected from the group consisting of neutral loss mass spectrometry and parent ion mass spectrometry.

117. (previously presented) The method of claim 116, comprising performing the neutral loss mass spectrometry or the parent ion mass spectrometry on a triple quadrupole mass spectrometer.

118 (previously presented) The method of claim 117, wherein performing the neutral loss mass spectrometry comprises:

- (a) scanning the product(s) of the enzymatic reaction and/or enzyme substrate in a first quadrupole at a specified mass range;
- (b) fragmenting the product(s) of the enzymatic reaction and/or enzyme substrate in a second quadrupole by collision induced dissociation, thereby producing one or more neutral fragments and one or more daughter ion; and,
- (c) detecting the one or more daughter ion.

119. (previously presented) The method of claim 117, wherein performing the parent ion mass spectrometry comprises:

- (a) scanning the product(s) of the enzymatic reaction and/or enzyme substrate in a first quadrupole;
- (b) fragmenting the product(s) of the enzymatic reaction and/or enzyme substrate in a second quadrupole by collision induced dissociation; and,
- (c) scanning a third quadrupole at a specified mass.

Claims 120-124 (canceled)

125. (previously presented) The method of claim 136, wherein an automatic sampler transports the samples from step (iv) to the mass spectrometer for injection and analysis at a rate of at least 100 samples an hour.

126. (previously presented) The method of claim 136, wherein 5 to 100 samples are pooled before performing flow-injection analysis using electrospray tandem mass spectrometry.

127. (previously presented) A method of performing high throughput mass spectrometry screening, the method comprising:

- (i) providing cells that have been transfected or transformed with one or more members of a library of related genes;
- (ii) growing the cells in vitro in a biological matrix to express said members of the library of related genes;
- (iii) separating the cells or cell debris thereof from one or more component of interest using centrifugation or filtration in a parallel fashion to provide samples comprising the component(s) of interest;
- (iv) performing flow-injection analysis using electrospray tandem mass spectrometry on the samples from step (iii) to obtain mass-to-charge ratio data for the component of interest, wherein the component(s) of interest is selected from the group consisting of an inorganic ion, a secondary metabolite, a protein binding molecule, a carbohydrate, a carbohydrate binding molecule, an enzyme, an enzyme substrate, a product of an enzyme catalyzed reaction, a nucleic acid, and a product of a nucleic acid catalyzed reaction, and wherein the component(s) of interest has not undergone chromatographic separation prior to step (iv).

128. (previously presented) The method of claim 127, wherein the cells are lysed prior to step (iii).

129. (previously presented) The method of claim 127, wherein the cells are permeabilized prior to step (iii).

130. (previously presented) The method of claim 127, wherein the component(s) of interest is obtained from cell supernatant.
131. (previously presented) The method of claim 127, wherein the component(s) of interest is a product of an enzymatic reaction.
132. (previously presented) The method of claim 127, wherein the cells are bacterial cells.
133. (previously presented) The method of claim 127, wherein the cells are eukaryotic cells.
134. (previously presented) The method of claim 127, wherein step (iii) is performed in a volatile buffer, a buffer that reduces concentration of ionic species, or an organic solvent.
135. (previously presented) The method of claim 131, further comprising simultaneously quantifying the amount of the product(s) of the enzymatic reaction and an enzyme substrate.
136. (currently amended) A method of performing high throughput mass spectrometry ~~spectrometry~~ screening, the method comprising:
- (i) providing cells that have been transfected or transformed with one or more members of a library of related enzyme encoding genes;
 - (ii) growing the cells in vitro in a biological matrix to express said members of the library of related enzyme encoding genes;
 - (iii) contacting the cells with one or more enzyme substrates to initiate formation of one or more products of an enzymatic reaction;

(iv) separating the cells or cell debris thereof from the product of the enzymatic reaction and/or enzyme substrate using centrifugation or filtration in a parallel fashion to provide samples comprising the product(s) of the enzymatic reaction and/or enzyme substrate(s); and

(v) performing flow-injection analysis using electrospray tandem mass spectrometry on the samples from step (iv) to obtain mass-to-charge ratio data for the product(s) of the enzymatic reaction and/or enzyme substrate(s),

wherein the product(s) of the enzymatic reaction and enzyme substrate(s) have not undergone chromatographic separation prior to step (v).

137. (previously presented) The method of claim 136, wherein the cells in step (iii) are lysed cells.

138. (previously presented) The method of claim 136, wherein the cells in step (iii) are permeabilized cells.

139. (previously presented) The method of claim 136, wherein the cells are bacterial cells.

140. (previously presented) The method of claim 136, wherein the cells are eukaryotic cells.

141. (previously presented) The method of claim 136, wherein step (iii) comprises using centrifugation.

142. (previously presented) The method of claim 136, wherein step (iii) comprises using filtration.

143. (previously presented) The method of claim 136, wherein step (iv) is performed in a volatile buffer, a buffer than reduces concentration of ionic species, or an organic solvent.

144. (new) The method of claim 136, wherein the component(s) of interest is obtained from cell supernatant.